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PATENT

REMARKS

Claims 36-50 have been cancelled herein. New claims 51-68 have been added. Support for the new claims can be found at, for example, page 12, lines 1-11, page 13, lines 4-13, page 15, lines 2-9 and in originally filed claims 23-25. No new matter has been added.

As a preliminary matter, Applicants' undersigned representative thanks the Examiner for the interview conducted on November 13, 2003. Applicants' representative would like to thank the Examiner for the opportunity to discuss the status of the claims under examination and to discuss the references cited in the Office Action.

I. The Claimed Invention Is Novel and Not Obvious

Claims 17-25 have been rejected as allegedly being anticipated by or obvious in view of some or all of the following references: 1) U.S. Patent No. 6,393,367, 2) U.S. Patent No. 6,055,487, 3) U.S. Patent No. 6,018,713, 4) Muddiman et al., Anal. Chem., 1997, 69, 1543-1549, and 5) Muddiman et al., Anal. Chem., 1996, 68, 3705-3712. Although Applicants maintain that claims 17-25 recited novel and non-obvious subject matter, claims 17-25 have been cancelled without prejudice to their presentation in another application.

New claims 51-68 recite a service for providing characterizing information about a bioagent. A database of base composition signatures that are indexed to molecular masses of amplification products of known bioagents is provided. The database is interrogated with an identification query comprising a measured molecular mass of a bioagent. The measured molecular mass is of an amplification product comprising a variable region that is present within a gene involved in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, energy generation, uptake, or secretion. The variable region is flanked by a pair of highly conserved regions. A response providing characterizing information for the bioagent that is generated by the database is delivered. Particular representative genes include, for example, DNA polymerase III beta, elongation factor TU, heat shock protein goEL, RNA polymerase beta, phosphoglycerate kinase, DADH dchydrogenase, DNA ligase, DNA topoisomerase, elongation factor G, and RNase P.